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BY:

*Allen Ito*

Date:

*August 1, 2006*

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

First Named Inventor:	Nobuya ITOH	§	Group Art Unit: 1652
		§	
Conf. No.:	7835	§	Examiner: Kagnew H. Gebreyesus, Ph.D.
		§	
Appln. No.:	10/782,998	§	Allowed May 2, 2006
		§	
Filing Date:	February 20, 2004	§	Attorney Docket No.: 600630-15US
		§	(562737)
Title:	REDUCTASE GENE AND USE OF THE SAME		

**DECLARATION OF HIROYUKI ASAKO**  
**REGARDING SECOND REPLACEMENT SEQUENCE LISTINGS**

I, Hiroyuki Asako, hereby declare as follows:

1. I am the research associate with Sumitomo Chemical Co., Ltd. ("Sumitomo"), the assignee of the rights in the above-identified patent application, based on an Assignment from the inventor, Nobuya Itoh, recorded in the U.S. Patent and Trademark Office on April 21, 2004, at Reel 015247, beginning at Frame 0239. I graduated with a Masters Degree from Tokyo Institute of Technology Department of Bioscience and Biotechnology in March, 1997. I began at Sumitomo in April, 1997 and have been engaged in biochemical research such as gene technology, fermentation, recombinant technology, bioconversion, and the like. I have been working with the inventor and Sumitomo's patent attorneys and am familiar with this application and its file history.

2. I was asked to review the application following receipt of the second Notice of Allowance dated May 2, 2006, prior to payment of the issue fee to make sure that the information in the application is accurate. Upon reviewing the Amended Sequence Listing filed

March 13, 2006, I realized that further corrections to the Sequence Listings for SEQ ID NOS:1 and 2 are needed.

3. The errors occurred as a result of yet further simple mistakes when reading the nucleotide sequence of SEQ ID NO:2 of the original gene of plasmid ptrTFAR that was analyzed with an ABI Prism 310 Genetic Analyzer, where the mistakes are identified as follows:

**(1) 123<sup>rd</sup> Nucleotide (123<sup>rd</sup> Original Nucleotide): Peak of "C" was buried by peak "A" due to succession of "A".**

**(2) 246<sup>th</sup> Nucleotide (246<sup>th</sup> Original Nucleotide): Peak of "C" was confirmed by performing analysis again. Same as original sequence.**

**(Correction made in the 1<sup>st</sup> Declaration turned out to be wrong)**

**(3) 467<sup>th</sup> Nucleotide (467<sup>th</sup> Original Nucleotide): Peak of "C" was buried by peak "G" due to continuation of "G" and "C".**

**(4) 575<sup>th</sup> Nucleotide (between 574<sup>th</sup> and 575<sup>th</sup> Original Nucleotide): Peak of "C" was buried due to continuation of "C" and low sensitivity of peak "C".**

**(5) 590<sup>th</sup> Nucleotide (between 588<sup>th</sup> and 589<sup>th</sup> Original Nucleotide): Peak of "C" was buried due to succession of "G" and "C" and low sensitivity of peak "C".**

**(6) 595<sup>th</sup> Nucleotide (593<sup>rd</sup> Original Nucleotide): Peak of "C" was buried due to succession of "T" and "C" and low sensitivity of peak "C".**

**(7) 597<sup>th</sup> Nucleotide (595<sup>th</sup> Original Nucleotide): Peak of "C" was buried due to succession of "T" and "C" and low sensitivity of peak "C".**

**(8) 619<sup>th</sup> Nucleotide (617<sup>th</sup> Original Nucleotide): Peak of "C" was buried by peak "T" due to continuation of "T" and "C".**

**(9) 622<sup>nd</sup> Nucleotide (620<sup>th</sup> Original Nucleotide): Peak of "G" was buried due to succession of "A" and "G" and low sensitivity of peak "G".**

**(10) 627<sup>th</sup> Nucleotide (between 624<sup>th</sup> and 625<sup>th</sup> Original Nucleotide): Peak of "C" was confirmed by performing analysis again.**

**(11) 695<sup>th</sup> Nucleotide (692<sup>nd</sup> Original Nucleotide): Peak of "A" was confirmed by performing analysis again. Same as original sequence.**

**(Correction made in the 1<sup>st</sup> Declaration turned out to be wrong)**

4. Attached is a copy of a ClustalW Formatted Alignments printout showing the nine mistakes identified in paragraph 3 above. Also attached is a comparison of the original and amended nucleotide sequence for SEQ ID NO:1, based on the corrections to the nucleotide sequence of SEQ ID NO:2.

5. The errors were inadvertent and without any disceptive intention.

6. Since the DNA of SEQ ID NO:2 is from the same *Leifsonia* sp. S-749 (Accession No. of International Depositary Authority: FERM BP-8291) and is the original gene of plasmid ptrTFAR as set forth in the application, no new matter has been added by correcting the nucleotide sequence of the DNA in SEQ ID NO:2.

7. In view of the corrections made to SEQ ID NO:2, the corresponding amino acids of SEQ ID NO:1 coded by the DNA of SEQ ID NO:2 also required correction. The corrections are noted in the attached comparison of the original amino acid sequence and the amended amino acid sequence for SEQ ID NO:1. For the same reasons as mentioned in paragraph 6, although corrections have been made to the amino acid sequence, no new matter has been added.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

**HIROYUKI ASAKO**

July 24, 2006  
(Date)

Hiroyuki Asako

## Original amino acid sequence

Met Ala Gln Tyr Asp Val Ala Asp Arg Ser Ala Ile Val Thr Gly Gly  
 1 5 10 15  
 Gly Ser Gly Ile Gly Arg Ala Val Ala Leu Thr Leu Ala Ala Ser Gly  
 20 25 30  
 Ala Ala Val Leu Val Thr Asp Leu **Lys** Glu Glu His Ala Gln Ala Val  
 35 40 45  
 Val Ala Glu Ile Glu Ala Ala Gly Lys Ala Ala Ala Leu Ala Gly  
 50 55 60  
 Asp Val Thr Asp Pro Ala Phe Gly Glu Ala Ser Val Ala Gly Ala Asn  
 65 70 75 80  
 Ala Leu Ala Pro Leu Lys Ile Ala Val Asn Asn Ala Gly Ile Gly Gly  
 85 90 95  
 Glu Ala Ala Thr Val Gly Asp Tyr Ser Leu Asp Ser Trp Arg Thr Val  
 100 105 110  
 Ile Glu Val Asn Leu Asn Ala Val Phe Tyr Gly Met Gln Pro Gln Leu  
 115 120 125  
 Lys Ala Met Ala Ala Asn Gly Gly Ala Ile Val Asn Met Ala Ser  
 130 135 140  
 Ile Leu Gly Ser Val Gly Phe Ala Asn Ser Ser **Gly** Tyr Val Thr Ala  
 145 150 155 160  
 Lys His Ala Leu Leu Gly Leu Thr Gln Asn Ala Ala Leu Glu Tyr Ala  
 165 170 175  
 Ala Asp Lys Val Arg Val Val Ala Val Gly Pro Gly Phe Ile Arg Thr  
 180 185 190  
**Arg** **Ser** **Trp** **Arg** **Gln** **Leu** **Phe** **Arg** **Arg** **Ala** **Gly** **Val** **Leu** **Gln** **Gly**  
 195 200 205  
 Lys His Ala Leu Gly Arg Leu Gly Glu Pro Glu Glu Val Ala Ser Leu  
 210 215 220  
 Val Ala Phe Leu Ala Ser Asp Ala Ala Ser Phe Ile Thr Gly Ser Tyr  
 225 230 235 240  
 His Leu Val Asp Gly Gly Tyr Thr Ala Gln  
 245 250

## Amended amino acid sequence

Met Ala Gln Tyr Asp Val Ala Asp Arg Ser Ala Ile Val Thr Gly Gly  
 1 5 10 15  
 Gly Ser Gly Ile Gly Arg Ala Val Ala Leu Thr Leu Ala Ala Ser Gly  
 20 25 30  
 Ala Ala Val Leu Val Thr Asp Leu **Asn** Glu Glu His Ala Gln Ala Val  
 35 40 45  
 Val Ala Glu Ile Glu Ala Ala Gly Lys Ala Ala Ala Leu Ala Gly  
 50 55 60  
 Asp Val Thr Asp Pro Ala Phe Gly Glu Ala Ser Val Ala Gly Ala Asn  
 65 70 75 80  
 Ala Leu Ala Pro Leu Lys Ile Ala Val Asn Asn Ala Gly Ile Gly Gly  
 85 90 95  
 Glu Ala Ala Thr Val Gly Asp Tyr Ser Leu Asp Ser Trp Arg Thr Val  
 100 105 110  
 Ile Glu Val Asn Leu Asn Ala Val Phe Tyr Gly Met Gln Pro Gln Leu  
 115 120 125  
 Lys Ala Met Ala Ala Asn Gly Gly Ala Ile Val Asn Met Ala Ser  
 130 135 140  
 Ile Leu Gly Ser Val Gly Phe Ala Asn Ser Ser **Ala** Tyr Val Thr Ala  
 145 150 155 160  
 Lys His Ala Leu Leu Gly Leu Thr Gln Asn Ala Ala Leu Glu Tyr Ala  
 165 170 175  
 Ala Asp Lys Val Arg Val Val Ala Val Gly Pro Gly Phe Ile Arg Thr  
 180 185 190  
**Pro** **Leu** **Val** **Glu** **Ala** **Asn** **Leu** **Ser** **Ala** **Asp** **Ala** **Leu** **Ala** **Phe** **Leu** **Glu**  
 195 200 205  
 Gly Lys His Ala Leu Gly Arg Leu Gly Glu Pro Glu Glu Val Ala Ser  
 210 215 220  
 Leu Val Ala Phe Leu Ala Ser Asp Ala Ala Ser Phe Ile Thr Gly Ser  
 225 230 235 240  
 Tyr His Leu Val Asp Gly Gly Tyr Thr Ala Gln  
 245 250

# SEQ ID NO:2

1: ATGGCTCAGTACGACGTCGCCACCGGTCCGCGATCGTGACCGGAGCGGCTCGGGCATC 60  
 1: ATGGCTCAGTACGACGTCGCCACCGGTCCGCGATCGTGACCGGAGCGGCTCGGGCATC 60  
 \*\*\*\*\*  
 61: GGGCGCGCGTGGCGCTCACTCTCGCGGCGAGCGGCGAGCCGCTCCTCGTCACCGACCTG 120  
 61: GGGCGCGCGTGGCGCTCACTCTCGCGGCGAGCGGCGAGCCGCTCCTCGTCACCGACCTG 120  
 \*\*\*\*\*  
 121: AATAGGAGCACGCGCAGCGCGTCTGTGGCCGAGATCGAGCCGCGGGCGGTAAAGCCCGCC 180  
 121: AATAGGAGCACGCGCAGCGCGTCTGTGGCCGAGATCGAGCCGCGGGCGGTAAAGCCCGCC 180  
 \*\*\*\*\*  
 181: GCGTCGCGGGCGACGTGACCGACCCCGCTTCGCGGAGCGAGCGTCGCGGGGCGAAC 240  
 181: GCGTCGCGGGCGACGTGACCGACCCCGCTTCGCGGAGCGAGCGTCGCGGGGCGAAC 240  
 \*\*\*\*\*  
 241: GCTCTCGCGCCCTCAAGATCGCGGTCAACACGCGGGCATCGGGCGAGGCCGCCACG 300  
 241: GCTCTCGCGCCCTCAAGATCGCGGTCAACACGCGGGCATCGGGCGAGGCCGCCACG 300  
 \*\*\*\*\*  
 301: GTCGGCGACTACTCGCTCGACAGCTGGCGCACGGTGATCGAGGTCAACCTCAACGCCGTG 360  
 301: GTCGGCGACTACTCGCTCGACAGCTGGCGCACGGTGATCGAGGTCAACCTCAACGCCGTG 360  
 \*\*\*\*\*  
 361: TTCTACGGGATCAGCGCAGCTGAAGCCATGGCCGCCAACCGCGCGGTGCGATCGTC 420  
 361: TTCTACGGGATCAGCGCAGCTGAAGCCATGGCCGCCAACCGCGCGGTGCGATCGTC 420  
 \*\*\*\*\*

Upper sequence : original nucleotide sequence

Lower sequence : amended nucleotide sequence

123A⇒C 467G⇒C 575 - ⇒C 590 ⇒C 595T⇒C 597T⇒C 619T⇒C 622A⇒G 627 ⇒C

421: AACATGGCGTCCATCTCTGGGAAGCGTCGGCTTCGCCAACTCGTCGGGTACGTACCGGCC 480  
 421: AACATGGCGTCCATCTCTGGGAAGCGTCGGCTTCGCCAACTCGTCGGGTACGTACCGGCC 480  
 \*\*\*\*\*  
 481: AAGCAGCGGTGCTCGGTCTCACCCAGAACCGCGCTCGAGTACGCCGCCGACAAGGTG 540  
 481: AAGCAGCGGTGCTCGGTCTCACCCAGAACCGCGCTCGAGTACGCCGCCGACAAGGTG 540  
 \*\*\*\*\*  
 541: CGCGTCGTGCGGTGCGGCCCGGCTTCATCCGCAACCGCTCGTGGAGGTAACCTTTCC 598  
 541: CGCGTCGTGCGGTGCGGCCCGGCTTCATCCGCAACCGCTCGTGGAGGTAACCTTTCC 598  
 \*\*\*\*\*  
 599: GCCGACGCGTGGCGTTCTCAAGGGTAAGCACGCCCTCGGCCCTGGGCGAGCCGGAA 657  
 599: GCCGACGCGTGGCGTTCTCAAGGGTAAGCACGCCCTCGGCCCTGGGCGAGCCGGAA 657  
 601: GCCGACGCGTGGCGTTCTCAAGGGTAAGCACGCCCTCGGCCCTGGGCGAGCCGGAA 660  
 601: GCCGACGCGTGGCGTTCTCAAGGGTAAGCACGCCCTCGGCCCTGGGCGAGCCGGAA 660  
 \*\*\*\*\*  
 658: GAGGTGCGCTCGTGGTGGTTCCTCGCTCCGACGCCGAGCTTCATCACCGGCAGC 717  
 658: GAGGTGCGCTCGTGGTGGTTCCTCGCTCCGACGCCGAGCTTCATCACCGGCAGC 717  
 661: GAGGTGCGCTCGTGGTGGTTCCTCGCTCCGACGCCGAGCTTCATCACCGGCAGC 720  
 661: GAGGTGCGCTCGTGGTGGTTCCTCGCTCCGACGCCGAGCTTCATCACCGGCAGC 720  
 \*\*\*\*\*  
 718: TACCACCTGGTGGACGGCGGTACACCGCCAGTGA 753  
 718: TACCACCTGGTGGACGGCGGTACACCGCCAGTGA 756  
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